# RAW SEQUENCE LISTING
## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/677,877*

Source: *IFWC*

Date Processed by STIC: *4/9/04*

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**
**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
*Effective 12/13/03*: TELEPHONE: 571-272-2510; FAX: 571-273-0221

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http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:
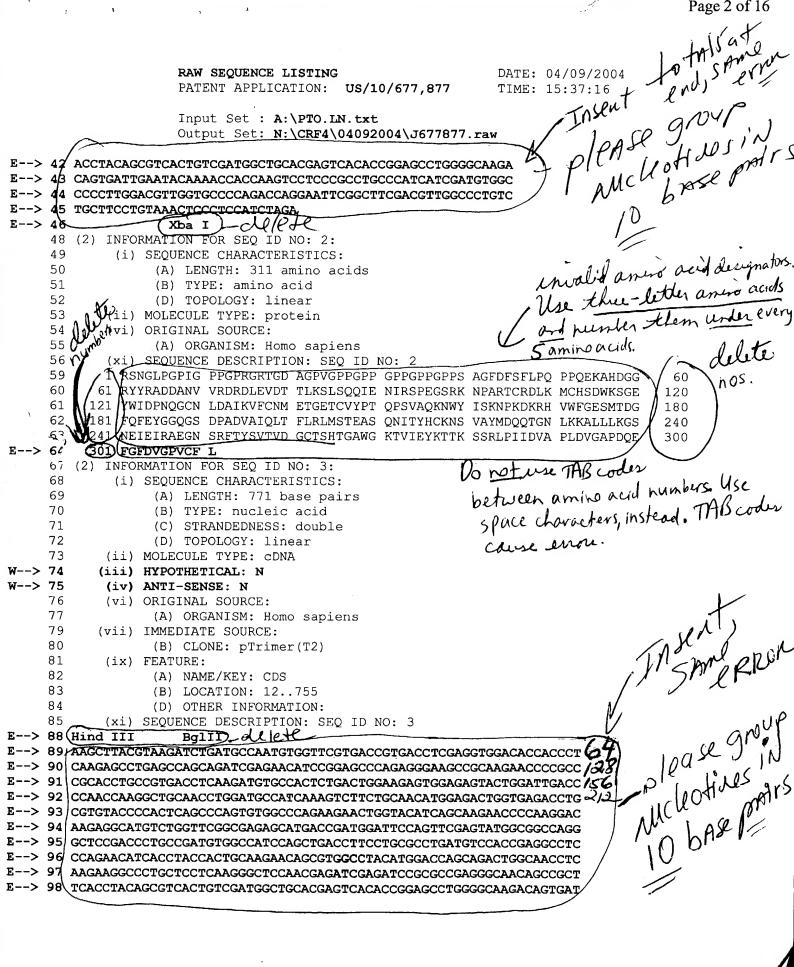
1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
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Revised 10/08/03

IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: **US/10/677,877**

DATE: 04/09/2004  
TIME: 15:37:16

Input Set : A:\PTO.LN.txt  
Output Set: N:\CRF4\04092004\J677877.raw

SEQUENCE LISTING

*Insert these Mandatory headings with Response:*  
*(I) Applicant:*  
*(II) Title of Invention:*

```
   3  (1) GENERAL INFORMATION:
   4     (iii) NUMBER OF SEQUENCES: 16          (insert)
C--> 0     (vi) CURRENT APPLICATION DATA:
C--> 0         (A) APPLICATION NUMBER: US/10/677,877
C--> 0         (B) FILING DATE: 02-Oct-2003
```

*(vi) CORRESPONDENCE ADDRESS:*  
*(A) ADDRESSEE:*  
*(B) STREET:*  
*(C) CITY:*  
*(D) STATE:*  
*(E) COUNTRY:*  
*(F) ZIP:*  
*(v) COMPUTER READABLE FORM:*  
*(A) MEDIUM TYPE:*  
*(B) COMPUTER:*  
*(C) OPERATING SYSTEM:*  
*(D) SOFTWARE:*  
*(vi) CURRENT APPLICATION DATA:*  
*(A) APPLICATION NUMBER:*  
*(B) FILING DATE:*

**ERRORED SEQUENCES**

```
   6  (2) INFORMATION FOR SEQ ID NO: 1:
   7     (i) SEQUENCE CHARACTERISTICS:
   8         (A) LENGTH: 963 base pairs
   9         (B) TYPE: nucleic acid
  10         (C) STRANDEDNESS: double
  11         (D) TOPOLOGY: linear
  12    (ii) MOLECULE TYPE: cDNA
W--> 13   (iii) HYPOTHETICAL: N
W--> 14   (iv) ANTI-SENSE: N
  15    (vi) ORIGINAL SOURCE:
  16         (A) ORGANISM: Homo sapiens
  18   (vii) IMMEDIATE SOURCE:
  19         (B) CLONE: pTrimer(T0)
  20    (ix) FEATURE:
  21         (A) NAME/KEY: CDS
  22         (B) LOCATION: 12..947
  23         (D) OTHER INFORMATION:
  24    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1
E--> 27  Hind III      BglII
E--> 28  AAGCTTACGTAAGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCG  55
E--> 29  CGGTCGCACTGGTGATGCTGGTCCTGTTGGTCCCCCCGGCCCTCCTGGACCTCCT 110
E--> 30  GGTCCCCCTGGTCCTCCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCAC 165
E--> 31  CTCAAGAGAAGGCTCACGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGT 220
E--> 32  GGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAGCCTGAGCCAGCAG
E--> 33  ATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAACCCCGCCCGCACCTGCC
E--> 34  GTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACCC
E--> 35  CAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGT
E--> 36  GAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCA
E--> 37  GCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGG
E--> 38  ATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAG
E--> 39  CTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACT
E--> 40  GCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCT
E--> 41  GCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTC
```

*Does Not Comply → (Pg. 1-15)*  
*Corrected Diskette Needed*

*Suggestion: Consult Sequence Rules for valid format.*

*✓ please insert Numbers at the end of sequence.*

*delete*

*✓ please group in 10 bases = each nucleotide*

*for ex: CGCAAGCTGT  |  AAGCTTACGT .......*

```
                    RAW SEQUENCE LISTING              DATE: 04/09/2004
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                    Input Set : A:\PTO.LN.txt
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E--> 42  ACCTACAGCGTCACTGTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGA
E--> 43  CAGTGATTGAATACAAAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGC
E--> 44  CCCCTTGGACGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTC
E--> 45  TGCTTCCTGTAAACTCCCTCCATCTAGA.
E--> 46             Xba I
     48  (2) INFORMATION FOR SEQ ID NO: 2:
     49      (i) SEQUENCE CHARACTERISTICS:
     50          (A) LENGTH: 311 amino acids
     51          (B) TYPE: amino acid
     52          (D) TOPOLOGY: linear
     53     (ii) MOLECULE TYPE: protein
     54     (vi) ORIGINAL SOURCE:
     55          (A) ORGANISM: Homo sapiens
     56     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2
     59    1 RSNGLPGPIG PPGPRGRTGD AGPVGPPGPP GPPGPPGPPS AGFDFSFLPQ PPQEKAHDGG    60
     60   61 RYYRADDANV VRDRDLEVDT TLKSLSQQIE NIRSPEGSRK NPARTCRDLK MCHSDWKSGE   120
     61  121 YWIDPNQGCN LDAIKVFCNM ETGETCVYPT QPSVAQKNWY ISKNPKDKRH VWFGESMTDG   180
     62  181 FQFEYGGQGS DPADVAIQLT FLRLMSTEAS QNITYHCKNS VAYMDQQTGN LKKALLLKGS   240
     63  241 NEIEIRAEGN SRFTYSVTVD GCTSHTGAWG KTVIEYKTTK SSRLPIIDVA PLDVGAPDQE   300
E--> 64  301 FGFDVGPVCF L
     67  (2) INFORMATION FOR SEQ ID NO: 3:
     68      (i) SEQUENCE CHARACTERISTICS:
     69          (A) LENGTH: 771 base pairs
     70          (B) TYPE: nucleic acid
     71          (C) STRANDEDNESS: double
     72          (D) TOPOLOGY: linear
     73     (ii) MOLECULE TYPE: cDNA
W--> 74    (iii) HYPOTHETICAL: N
W--> 75     (iv) ANTI-SENSE: N
     76     (vi) ORIGINAL SOURCE:
     77          (A) ORGANISM: Homo sapiens
     79    (vii) IMMEDIATE SOURCE:
     80          (B) CLONE: pTrimer(T2)
     81     (ix) FEATURE:
     82          (A) NAME/KEY: CDS
     83          (B) LOCATION: 12..755
     84          (D) OTHER INFORMATION:
     85     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3
E--> 88  Hind III        BglII
E--> 89  AAGCTTACGTAAGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCT   64
E--> 90  CAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAACCCCGCC  128
E--> 91  CGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATTGACC  156
E--> 92  CCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTG  2??
E--> 93  CGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGAC
E--> 94  AAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGG
E--> 95  GCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTC
E--> 96  CCAGAACATCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTC
E--> 97  AAGAAGGCCCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCT
E--> 98  TCACCTACAGCGTCACTGTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGAT
```

Handwritten annotations:
- Insert totals at end, same error
- please group nucleotides in base pairs 10
- invalid amino acid designators. Use three-letter amino acids and number them under every 5 amino acids.
- delete nos.
- delete numbers
- Do not use TAB codes between amino acid numbers. Use space characters, instead. TAB codes cause error.
- delete (Xba I)
- delete (Hind III BglII)
- Insert, same error
- please group nucleotides in 10 base pairs
- 64, 128, 156, 2??

```
                    RAW SEQUENCE LISTING              DATE: 04/09/2004
                    PATENT APPLICATION:  US/10/677,877  TIME: 15:37:16

                    Input Set : A:\PTO.LN.txt
                    Output Set: N:\CRF4\04092004\J677877.raw
```

*(handwritten: Insert totals at end. — same error)*

```
E--> 99  TGAATACAAAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGT
E--> 100 GCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAACTCCCTCCATCT
E--> 101 AGA
E--> 102 Xba I        *(handwritten: delete)*
    105 (2) INFORMATION FOR SEQ ID NO: 4:
    106      (i) SEQUENCE CHARACTERISTICS:
    107          (A) LENGTH: 247 amino acids
    108          (B) TYPE: amino acid
    109          (D) TOPOLOGY: linear
    110     (ii) MOLECULE TYPE: protein
    111     (vi) ORIGINAL SOURCE:
    112          (A) ORGANISM: Homo sapiens
    113    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4
```

*(handwritten: delete nos.)*  *(handwritten: same error as sequence 2)*  *(handwritten: delete)*

```
    116   1  RSDANVVRDR DLEVDTTLKS LSQQIENIRS PEGSRKNPAR TCRDLKMCHS DWKSGEYWID   60
    117  61  PNQGCNLDAI KVFCNMETGE TCVYPTQPSV AQKNWYISKN PKDKRHVWFG ESMTDGFQFE  120
    118 121  YGGQGSDPAD VAIQLTFLRL MSTEASQNIT YHCKNSVAYM DQQTGNLKKA LLLKGSNEIE  180
    119 181  IRAEGNSRFT YSVTVDGCTS HTGAWGKTVI EYKTTKSSRL PIIDVAPLDV GAPDQEFGFD  240
E--> 120 241 VGPVCFL
    123 (2) INFORMATION FOR SEQ ID NO: 5:
    124      (i) SEQUENCE CHARACTERISTICS:
    125          (A) LENGTH: 2487 base pairs
    126          (B) TYPE: nucleic acid
    127          (C) STRANDEDNESS: double
    128          (D) TOPOLOGY: linear
    129     (ii) MOLECULE TYPE: cDNA
W--> 130    (iii) HYPOTHETICAL: N
W--> 131     (iv) ANTI-SENSE: N
    132     (vi) ORIGINAL SOURCE:
    133          (A) ORGANISM: Homo sapiens
    135    (vii) IMMEDIATE SOURCE:
    136          (B) CLONE: pTrimer/AP-T0
    137     (ix) FEATURE:
    138          (A) NAME/KEY: CDS
    139          (B) LOCATION: 12..2471
    140          (D) OTHER INFORMATION:
    141    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5
```

*(handwritten: Insert totals — same error)*

```
E--> 144 Hind III   *(handwritten: delete)*
E--> 145 AAGCTTCCTGCATGCTGCTGCTGCTGCTGCTGGGCCTGAGGCTACAGCTCTCCCTG    59
E--> 146 GGCATCATCCCAGTTGAGGAGGAGAACCCGGACTTCTGGAACCGCGAGGCAGCCGAGGC   118
E--> 147 CCTGGGTGCCGCCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCTCATCATCT   236
E--> 148 TCCTGGGCGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCCTAAAAGGGCAG
E--> 149 AAGAAGGACAAACTGGGGCCTGAGATACCCCTGGCCATGGACCGCTTCCCATATGTGGC
E--> 150 TCTGTCCAAGACATACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGG
E--> 151 CCTACCTGTGCGGGGTCAAGGGCAACTTCCAGACCATTGGCTTGAGTGCAGCCGCCCGC
E--> 152 TTTAACCAGTGCAACACGACACGCGGCAACGAGGTCATCTCCGTGATGAATCGGGCCAA
E--> 153 GAAAGCAGGGAAGTCAGTGGGAGTGGTAACCACCACACGAGTGCAGCACGCCTCGCCAG
E--> 154 CCGGCACCTACGCCCACACGGTGAACCGCAACTGGTACTCGGACGCCGACGTGCCTGCC
E--> 155 TCGGCCCGCCAGGAGGGGTGCCAGGACATCGCTACGCAGCTCATCTCCAACATGGACAT
E--> 156 TGACGTGATCCTAGGTGGAGGCCGAAAGTACATGTTTCCCATGGGAACCCCAGACCCTG
```

Input Set : A:\PTO.LN.txt
Output Set: N:\CRF4\04092004\J677877.raw

*Insert totals at end.*

*— same errors*

```
E--> 157  AGTACCCAGATGACTACAGCCAAGGTGGGACCAGGCTGGACGGGAAGAATCTGGTGCAG
E--> 158  GAATGGCTGGCGAAGCGCCAGGGTGCCCGGTATGTGTGGAACCGCACTGAGCTCATGCA
E--> 159  GGCTTCCCTGGACCCGTCTGTGACCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGA
E--> 160  AATACGAGATCCACCGAGACTCCACACTGGACCCCTCCCTGATGGAGATGACAGAGGCT
E--> 161  GCCCTGCGCCTGCTGAGCAGGAACCCCCGCGGCTTCTTCCTCTTCGTGGAGGGTGGTCG
E--> 162  CATCGACCATGGTCATCATGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGT
E--> 163  TCGACGACGCCATTGAGAGGGCGGGCCAGCTCACCAGCGAGGAGGACACGCTGAGCCTC
E--> 164  GTCACTGCCGACCACTCCCACGTCTTCTCCTTCGGAGGCTACCCCCTGCGAGGGAGCTC
E--> 165  CATCTTCGGGCTGGCCCCTGGCAAGGCCCGGGACAGGAAGGCCTACACGGTCCTCCTAT
E--> 166  ACGGAAACGGTCCAGGCTATGTGCTCAAGGACGGCGCCCGGCCGGATGTTACCGAGAGC
E--> 167  GAGAGCGGGAGCCCCGAGTATCGGCAGCAGTCAGCAGTGCCCCTGGACGAAGAGACCCA
E--> 168  CGCAGGCGAGGACGTGGCGGTGTTCGCGCGCGGCCCGCAGGCGCACCTGGTTCACGGCG
E--> 169  TGCAGGAGCAGACCTTCATAGCGCACGTCATGGCCTTCGCCGCCTGCCTGGAGCCCTAC
E--> 170  ACCGCCTGCGACCTGGCGCCCCCCGCCGGCACCACCGACGCCGCGCACCCGGGTTCCGG
E--> 171  AAGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCACTGGTG
E--> 172  ATGCTGGTCCTGTTGGTCCCCCCGGCCCTCCTGGACCTCCTGGTCCCCCTGGTCCTCCC
E--> 173  AGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCACGATGG
E--> 174  TGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGG
E--> 175  ACACCACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGC
E--> 176  CGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAG
E--> 177  TGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCT
E--> 178  GCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAG
E--> 179  AACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCAT
E--> 180  GACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCA
E--> 181  TCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCAC
E--> 182  TGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCT
E--> 183  CCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACA
E--> 184  GCGTCACTGTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAA
E--> 185  TACAAAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCCTTGGACGTTGG
E--> 186  TGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAACTCCCT
E--> 187  CCATCTAGA
E--> 188  Xba I  delete
```

```
191  (2) INFORMATION FOR SEQ ID NO: 6:
192       (i) SEQUENCE CHARACTERISTICS:
193            (A) LENGTH: 819 amino acids
194            (B) TYPE: amino acid
195            (D) TOPOLOGY: linear
196       (ii) MOLECULE TYPE: protein
197       (vi) ORIGINAL SOURCE:
198            (A) ORGANISM: Homo sapiens
199       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6
```

*delete #s* *— same errors*

```
202    1  MLLLLLLLGL RLQLSLGIIP VEEENPDFWN REAAEALGAA KKLQPAQTAA KNLIIFLGDG   60
203   61  MGVSTVTAAR ILKGQKKDKL GPEIPLAMDR FPYVALSKTY NVDKHVPDSG ATATAYLCGV  120
204  121  KGNFQTIGLS AAARFNQCNT TRGNEVISVM NRAKKAGKSV GVVTTTRVQH ASPAGTYAHT  180
205  181  VNRNWYSDAD VPASARQEGC QDIATQLISN MDIDVILGGG RKYMFPMGTP DPEYPDDYSQ  240
206  241  GGTRLDGKNL VQEWLAKRQG ARYVWNRTEL MQASLDPSVT HLMGLFEPGD MKYEIHRDST  300
207  301  LDPSLMEMTE AALRLLSRNP RGFFLFVEGG RIDHGHHESR AYRALTETIM FDDAIERAGQ  360
208  361  LTSEEDTLSL VTADHSHVFS FGGYPLRGSS IFGLAPGKAR DRKAYTVLLY GNGPGYVLKD  420
209  421  GARPDVTESE SGSPEYRQQS AVPLDEETHA GEDVAVFARG PQAHLVHGVQ EQTFIAHVMA  480
```

*delete #s*

RAW SEQUENCE LISTING
PATENT APPLICATION:  **US/10/677,877**

DATE: 04/09/2004
TIME: 15:37:16

*same errors*

*delete #S*

*delete #S*

Input Set : **A:\PTO.LN.txt**
Output Set: **N:\CRF4\04092004\J677877.raw**

```
      210    481 FAACLEPYTA CDLAPPAGTT DAAHPGSGRS NGLPGPIGPP GPRGRTGDAG PVGPPGPPGP    540
      211    541 PGPPGPPSAG FDFSFLPQPP QEKAHDGGRY YRADDANVVR DRDLEVDTTL KSLSQQIENI    600
      212    601 RSPEGSRKNP ARTCRDLKMC HSDWKSGEYW IDPNQGCNLD AIKVFCNMET GETCVYPTQP    660
      213    661 SVAQKNWYIS KNPKDKRHVW FGESMTDGFQ FEYGGQGSDP ADVAIQLTFL RLMSTEASQN    720
      214    721 ITYHCKNSVA YMDQQTGNLK KALLLKGSNE IEIRAEGNSR FTYSVTVDGC TSHTGAWGKT    780
E--> 215    781 VIEYKTTKSS RLPIIDVAPL DVGAPDQEFG FDVGPVCFL
      218 (2) INFORMATION FOR SEQ ID NO: 7:
      219        (i) SEQUENCE CHARACTERISTICS:
      220            (A) LENGTH: 2294 base pairs
      221            (B) TYPE: nucleic acid
      222            (C) STRANDEDNESS: double
      223            (D) TOPOLOGY: linear
      224       (ii) MOLECULE TYPE: cDNA
W--> 225      (iii) HYPOTHETICAL: N
W--> 226       (iv) ANTI-SENSE: N
      227       (vi) ORIGINAL SOURCE:
      228            (A) ORGANISM: Homo sapiens
      230      (vii) IMMEDIATE SOURCE:
      231            (B) CLONE: pTrimer/AP-T2
      232       (ix) FEATURE:
      233            (A) NAME/KEY: CDS
      234            (B) LOCATION: 12..2278
      235            (D) OTHER INFORMATION:
      236       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7
E--> 238 Hind III  delete
E--> 239 AAGCTTCCTGCATGCTGCTGCTGCTGCTGCTGGGCCTGAGGCTACAGCTCTCCCTG
E--> 240 GGCATCATCCCAGTTGAGGAGGAGAACCCGGACTTCTGGAACCGCGAGGCAGCCGAGGC
E--> 241 CCTGGGTGCCGCCAAGAAGCTGCAGCCTGCACAGACAGCCGCCAAGAACCTCATCATCT
E--> 242 TCCTGGGCGATGGGATGGGGGTGTCTACGGTGACAGCTGCCAGGATCCTAAAAGGGCAG
E--> 243 AAGAAGGACAAACTGGGGCCTGAGATACCCCTGGCCATGGACCGCTTCCCATATGTGGC
E--> 244 TCTGTCCAAGACATACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGG
E--> 245 CCTACCTGTGCGGGGTCAAGGGCAACTTCCAGACCATTGGCTTGAGTGCAGCCGCCCGC
E--> 246 TTTAACCAGTGCAACACGACACGCGGCAACGAGGTCATCTCCGTGATGAATCGGGCCAA
E--> 247 GAAAGCAGGGAAGTCAGTGGGAGTGGTAACCACCACACGAGTGCAGCACGCCTCGCCAG
E--> 248 CCGGCACCTACGCCCACACGGTGAACCGCAACTGGTACTCGGACGCCGACGTGCCTGCC
E--> 249 TCGGCCCGCCAGGAGGGGTGCCAGGACATCGCTACGCAGCTCATCTCCAACATGGACAT
E--> 250 TGACGTGATCCTAGGTGGAGGCCGAAAGTACATGTTTCCCATGGGAACCCCAGACCCTG
E--> 251 AGTACCAGATGACTACAGCCAAGGTGGGACCAGGCTGGACGGGAAGAATCTGGTGCAG
E--> 252 GAATGGCTGGCGAAGCGCCAGGGTGCCCGGTATGTGTGGAACCGCACTGAGCTCATGCA
E--> 253 GGCTTCCCTGGACCCGTCTGTGACCCATCTCATGGGTCTCTTTGAGCCTGGAGACATGA
E--> 254 AATACGAGATCCACCGAGACTCCACACTGGACCCCTCCCTGATGGAGATGACAGAGGCT
E--> 255 GCCCTGCGCCTGCTGAGCAGGAACCCCCGCGGCTTCTTCCTCTTCGTGGAGGGTGGTCG
E--> 256 CATCGACCATGGTCATCATGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGT
E--> 257 TCGACGACGCCATTGAGAGGGCGGGCCAGCTCACCAGCGAGGAGGACACGCTGAGCCTC
E--> 258 GTCACTGCCGACCACTCCCACGTCTTCTCCTTCGGAGGCTACCCCCTGCGAGGGAGCTC
E--> 259 CATCTTCGGGCTGGCCCCTGGCAAGGCCCGGGACAGGAAGGCCTACACGGTCCTCCTAT
E--> 260 ACGGAAACGGTCCAGGCTATGTGCTCAAGGACGGCGCCCGGCCGGATGTTACCGAGAGC
E--> 261 GAGAGCGGGAGCCCCGAGTATCGGCAGCAGTCAGCAGTGCCCCTGGACGAAGAGACCCA
E--> 262 CGCAGGCGAGGACGTGGCGGTGTTCGCGCGCGGCCCGCAGGCGCACCTGGTTCACGGCG
```

*Insert totals at end.*

*same errors*

```
RAW SEQUENCE LISTING                    DATE: 04/09/2004
PATENT APPLICATION:  US/10/677,877      TIME: 15:37:16

        Input Set : A:\PTO.LN.txt
        Output Set: N:\CRF4\04092004\J677877.raw
```

```
E--> 263  TGCAGGAGCAGACCTTCATAGCGCACGTCATGGCCTTCGCCGCCTGCCTGGAGCCCTAC
E--> 264  ACCGCCTGCGACCTGGCGCCCCCCGCCGGCACCACCGACGCCGCGCACCCGGGTTCCGG
E--> 265  AGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCCTCAAGAG
E--> 266  CCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAACCCCGCCC
E--> 267  GCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTACTGGATT
E--> 268  GACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGGAGACTGG
E--> 269  TGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTACATCAGCA
E--> 270  AGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGGATTCCAG
E--> 271  TTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGACCTTCCT
E--> 272  GCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAACAGCGTGG
E--> 273  CCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTCAAGGGCTCCAAC
E--> 274  GAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTGTCGATGG
E--> 275  CTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACCACCAAGT
E--> 276  CCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGACCAGGAA
E--> 277  TTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAACTCCCTCCATCTAGA
E--> 278                Xba I
     281  (2) INFORMATION FOR SEQ ID NO: 8:
     282          (i) SEQUENCE CHARACTERISTICS:
     283               (A) LENGTH: 755 amino acids
     284               (B) TYPE: amino acid
     285               (D) TOPOLOGY: linear
     286         (ii) MOLECULE TYPE: protein
     287         (vi) ORIGINAL SOURCE:
     288               (A) ORGANISM: Homo sapiens
     289         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8
     292     1 MLLLLLLLGL RLQLSLGIIP VEEENPDFWN REAAEALGAA KKLQPAQTAA KNLIIFLGDG   60
     293    61 MGVSTVTAAR ILKGQKKDKL GPEIPLAMDR FPYVALSKTY NVDKHVPDSG ATATAYLCGV  120
     294   121 KGNFQTIGLS AAARFNQCNT TRGNEVISVM NRAKKAGKSV GVVTTTRVQH ASPAGTYAHT  180
     295   181 VNRNWYSDAD VPASARQEGC QDIATQLISN MDIDVILGGG RKYMFPMGTP DPEYPDDYSQ  240
     296   241 GGTRLDGKNL VQEWLAKRQG ARYVWNRTEL MQASLDPSVT HLMGLFEPGD MKYEIHRDST  300
     297   301 LDPSLMEMTE AALRLLSRNP RGFFLFVEGG RIDHGHHESR AYRALTETIM FDDAIERAGQ  360
     298   361 LTSEEDTLSL VTADHSHVFS FGGYPLRGSS IFGLAPGKAR DRKAYTVLLY GNGPGYVLKD  420
     299   421 GARPDVTESE SGSPEYRQQS AVPLDEETHA GEDVAVFARG PQAHLVHGVQ EQTFIAHVMA  480
     300   481 FAACLEPYTA CDLAPPAGTT DAAHPGSGRS DANVVRDRDL EVDTTLKSLS QQIENIRSPE  540
     301   541 GSRKNPARTC RDLKMCHSDW KSGEYWIDPN QGCNLDAIKV FCNMETGETC VYPTQPSVAQ  600
     302   601 KNWYISKNPK DKRHVWFGES MTDGFQFEYG GQGSDPADVA IQLTFLRLMS TEASQNITYH  660
     303   661 CKNSVAYMDQ QTGNLKKALL LKGSNEIEIR AEGNSRFTYS VTVDGCTSHT GAWGKTVIEY  720
E--> 304   721 KTTKSSRLPI IDVAPLDVGA PDQEFGFDVG PVCFL
     307  (2) INFORMATION FOR SEQ ID NO: 9:
     308          (i) SEQUENCE CHARACTERISTICS:
     309               (A) LENGTH: 1734 base pairs
     310               (B) TYPE: nucleic acid
     311               (C) STRANDEDNESS: double
     312               (D) TOPOLOGY: linear
     313         (ii) MOLECULE TYPE: cDNA
W--> 314        (iii) HYPOTHETICAL: N
W--> 315         (iv) ANTI-SENSE: N
     316         (vi) ORIGINAL SOURCE:
     317               (A) ORGANISM: Homo sapiens
```

RAW SEQUENCE LISTING          DATE: 04/09/2004
PATENT APPLICATION: **US/10/677,877**    TIME: 15:37:16

Input Set : **A:\PTO.LN.txt**
Output Set: **N:\CRF4\04092004\J677877.raw**

```
319      (vii)  IMMEDIATE SOURCE:
320             (B)  CLONE: pTrimer/sTNFRII-T0
321      (ix)  FEATURE:
322             (A)  NAME/KEY: CDS
323             (B)  LOCATION: 18..1718
324             (D)  OTHER INFORMATION:
325      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 9
E--> 327  Bam HI — delete
E--> 328  GGATCCCGCCCGCACCCATGGCGCCCGTCGCCGTCTGGGCCGCGCTGGCCGTCGGACTGGAGCT
E--> 329  CTGGGCTGCGGCGCACGCCTTGCCCGCCCAGGTGGCATTTACACCCTACGCCCCGGAGCCCGGG
E--> 330  AGCACATGCCGGCTCAGAGAATACTATGACCAGACAGCTCAGATGTGCTGCAGCAAATGCTCGC
E--> 331  CGGGCCAACATGCAAAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAGGA
E--> 332  CAGCACATACACCCAGCTCTGGAACTGGGTTCCCGAGTGCTTGAGCTGTGGCTCCCGCTGTAGC
E--> 333  TCTGACCAGGTGGAAACTCAAGCCTGCACTCGGGAACAGAACCGCATCTGCACCTGCAGGCCCG
E--> 334  GCTGGTACTGCGCGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAGTGCCG
E--> 335  CCCGGGCTTCGGCGTGGCCAGACCAGGAACTGAAACATCAGACGTGGTGTGCAAGCCCTGTGCC
E--> 336  CCGGGGACGTTCTCCAACACGACTTCATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACG
E--> 337  TGGTGGCCATCCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCACCCGGAG
E--> 338  TATGGCCCCAGGGGCAGTACACTTACCCCAGCCAGTGTCCACACGATCCCAACACACGCAGCCA
E--> 339  ACTCCAGAACCCAGCACTGCTCCAAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCCAG
E--> 340  CTGAAGGGAGCACTGGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGG
E--> 341  TCGCACTGGTGATGCTGGTCCTGTTGGTCCCCCCGGCCCTCCTGGACCTCCTGGTCCCC
E--> 342  CTGGTCCTCCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAG
E--> 343  GCTCACGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGA
E--> 344  CCTCGAGGTGGACACCCACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCC
E--> 345  CAGAGGGAAGCCGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCT
E--> 346  GACTGGAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCAT
E--> 347  CAAAGTCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTG
E--> 348  TGGCCCAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTC
E--> 349  GGCGAGAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGC
E--> 350  CGATGTGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACA
E--> 351  TCACCTACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAG
E--> 352  AAGGCCCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCG
E--> 353  CTTCACCTACAGCGTCACTGTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGA
E--> 354  CAGTGATTGAATACAAAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCC
E--> 355  TTGGACGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCT
E--> 356  GTAAAGTCCCTCCATCTAGA
E--> 357  Xba I — delete
360  (2)  INFORMATION FOR SEQ ID NO: 10:
361       (i)  SEQUENCE CHARACTERISTICS:
362            (A)  LENGTH: 566 amino acids
363            (B)  TYPE: amino acid
364            (D)  TOPOLOGY: linear
365       (ii)  MOLECULE TYPE: protein
366       (vi)  ORIGINAL SOURCE:
367            (A)  ORGANISM: Homo sapiens
368       (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 10
371   1  MAPVAVWAAL AVGLELWAAA HALPAQVAFT PYAPEPGSTC RLREYYDQTA QMCCSKCSPG   60
372  61  QHAKVFCTKT SDTVCDSCED STYTQLWNWV PECLSCGSRC SSDQVETQAC TREQNRICTC  120
```

*(handwritten margin notes: "✓ Insert to tags at end.", "← same errors", "✓ same errors", "— delete #s", "delete #s")*

*delete* (handwritten)

**RAW SEQUENCE LISTING**
PATENT APPLICATION: **US/10/677,877**

DATE: 04/09/2004
TIME: 15:37:16

*Same errors* (handwritten)

Input Set : **A:\PTO.LN.txt**
Output Set: **N:\CRF4\04092004\J677877.raw**

*delete* (handwritten)

```
373  121 RPGWYCALSK QEGCRLCAPL RKCRPGFGVA RPGTETSDVV CKPCAPGTFS NTTSSTDICR  180
374  181 PHQICNVVAI PGNASMDAVC TSTSPTRSMA PGAVHLPQPV STRSQHTQPT PEPSTAPSTS  240
375  241 FLLPMGPSPP AEGSTGSNGL PGPIGPPGPR GRTGDAGPVG PPGPPGPPGP PGPPSAGFDF  300
376  301 SFLPQPPQEK AHDGGRYYRA DDANVVRDRD LEVDTTLKSL SQQIENIRSP EGSRKNPART  360
377  361 CRDLKMCHSD WKSGEYWIDP NQGCNLDAIK VFCNMETGET CVYPTQPSVA QKNWYISKNP  420
378  421 KDKRHVWFGE SMTDGFQFEY GGQGSDPADV AIQLTFLRLM STEASQNITY HCKNSVAYMD  480
379, 481 QQTGNLKKAL LLKGSNEIEI RAEGNSRFTY SVTVDGCTSH TGAWGKTVIE YKTTKSSRLP  540
E--> 380  541 IIDVAPLDVG APDQEFGFDV GPVCFL
383  (2) INFORMATION FOR SEQ ID NO: 11:
384      (i) SEQUENCE CHARACTERISTICS:
385          (A) LENGTH: 1542 base pairs
386          (B) TYPE: nucleic acid
387          (C) STRANDEDNESS: double
388          (D) TOPOLOGY: linear
389     (ii) MOLECULE TYPE: cDNA
W--> 390  (iii) HYPOTHETICAL: N
W--> 391   (iv) ANTI-SENSE: N
392     (vi) ORIGINAL SOURCE:
393          (A) ORGANISM: Homo sapiens
395    (vii) IMMEDIATE SOURCE:
396          (B) CLONE: pTrimer/sTNFRII-T2
397     (ix) FEATURE:
398          (A) NAME/KEY: CDS
399          (B) LOCATION: 18..1526
400          (D) OTHER INFORMATION:
401     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11
E--> 404 Bam HI   delete
E--> 405 GGATCCCGCCCGCACCCATGGCGCCCGTCGCCGTCTGGGCCGCGCTGGCCGTCGGACTGGAGCT  64
E--> 406 CTGGGCTGCGGCGCACGCCTTGCCCGCCCAGGTGGCATTTACACCCTACGCCCCGGAGCCCGGG
E--> 407 AGCACATGCCGGCTCAGAGAATACTATGACCAGACAGCTCAGATGTGCTGCAGCAAATGCTCGC
E--> 408 CGGGCCAACATGCAAAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAGGA
E--> 409 CAGCACATACACCCAGCTCTGGAACTGGGTTCCCGAGTGCTTGAGCTGTGGCTCCCGCTGTAGC
E--> 410 TCTGACCAGGTGGAAACTCAAGCCTGCACTCGGGAACAGAACCGCATCTGCACCTGCAGGCCCG
E--> 411 GCTGGTACTGCGCGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAGTGCCG
E--> 412 CCCCGGGCTTCGGCGTGGCCAGACCAGGAACTGAAACATCAGACGTGGTGTGCAAGCCCTGTGCC
E--> 413 CCGGGGACGTTCTCCAACACGACTTCATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACG
E--> 414 TGGTGGCCATCCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCACCCGGAG
E--> 415 TATGGCCCCAGGGGCAGTACACTTACCCCAGCCAGTGTCCACACGATCCCAACACACGCAGCCA
E--> 416 ACTCCAGAACCCAGCACTGCTCCAAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCCAG
E--> 417 CTGAAGGGAGCACTGGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACAC
E--> 418 CACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCA
E--> 419 AGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGA
E--> 420 GAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAA
E--> 421 CATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACT
E--> 422 GGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACC
E--> 423 GATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCA
E--> 424 GCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACTGCA
E--> 425 AGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTC
E--> 426 AAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACAGCGT
```

*Insert totals at end* (handwritten)

*SAME errors* (handwritten)

RAW SEQUENCE LISTING                    DATE: 04/09/2004
PATENT APPLICATION:  US/10/677,877      TIME: 15:37:16

Input Set : A:\PTO.LN.txt
Output Set: N:\CRF4\04092004\J677877.raw

*(handwritten: ✓ Insert totals — same errors)*

```
E--> 427  CACTGTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACA
E--> 428  AAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCC
E--> 429  CCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAACTCCCTCCAT
E--> 430  CTAGA
E--> 431  Xba I   delete
     434  (2) INFORMATION FOR SEQ ID NO: 12:
     435       (i) SEQUENCE CHARACTERISTICS:
     436           (A) LENGTH: 502 amino acids
     437           (B) TYPE: amino acid
     438           (D) TOPOLOGY: linear
     439      (ii) MOLECULE TYPE: protein
     440      (vi) ORIGINAL SOURCE:
     441           (A) ORGANISM: Homo sapiens
     442      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12
     445    1  MAPVAVWAAL AVGLELWAAA HALPAQVAFT PYAPEPGSTC RLREYYDQTA QMCCSKCSPG   60
     446   61  QHAKVFCTKT SDTVCDSCED STYTQLWNWV PECLSCGSRC SSDQVETQAC TREQNRICTC  120
     447  121  RPGWYCALSK QEGCRLCAPL RKCRPGFGVA RPGTETSDVV CKPCAPGTFS NTTSSTDICR  180
     448  181  PHQICNVVAI PGNASMDAVC TSTSPTRSMA PGAVHLPQPV STRSQHTQPT PEPSTAPSTS  240
     449  241  FLLPMGPSPP AEGSTGSDAN VVRDRDLEVD TTLKSLSQQI ENIRSPEGSR KNPARTCRDL  300
     450  301  KMCHSDWKSG EYWIDPNQGC NLDAIKVFCN METGETCVYP TQPSVAQKNW YISKNPKDKR  360
     451  361  HVWFGESMTD GFQFEYGGQG SDPADVAIQL TFLRLMSTEA SQNITYHCKN SVAYMDQQTG  420
     452  421  NLKKALLLKG SNEIEIRAEG NSRFTYSVTV DGCTSHTGAW GKTVIEYKTT KSSRLPIIDV  480
E--> 453  481  APLDVGAPDQ EFGFDVGPVC FL
     456  (2) INFORMATION FOR SEQ ID NO: 13:
     457       (i) SEQUENCE CHARACTERISTICS:
     458           (A) LENGTH: 2139 base pairs
     459           (B) TYPE: nucleic acid
     460           (C) STRANDEDNESS: double
     461           (D) TOPOLOGY: linear
     462      (ii) MOLECULE TYPE: cDNA
W--> 463     (iii) HYPOTHETICAL: N
W--> 464     (iv) ANTI-SENSE: N
     465      (vi) ORIGINAL SOURCE:
     466           (A) ORGANISM: Homo sapiens
     468     (vii) IMMEDIATE SOURCE:
     469           (B) CLONE: pTrimer/sCD4-T0
     470      (ix) FEATURE:
     471           (A) NAME/KEY: CDS
     472           (B) LOCATION: 24..2123
     473           (D) OTHER INFORMATION:
     474      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13
E--> 477  Hind III   delete
E--> 478  AAGCTTCCCTCGGCAAGGCCACAATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTG
E--> 479  GTGCTGCAACTGGCGCTCCTCCCAGCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAA
E--> 480  AAAAGGGGATACAGTGGAACTGACCTGTACAGCTTCCCAGAAGAAGAGCATACAATTCC
E--> 481  ACTGGAAAAACTCCAACCAGATAAAGATTCTGGGAAATCAGGGCTCCTTCTTAACTAAA
E--> 482  GGTCCATCCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCTTTGGGACCAAGGAAA
E--> 483  CTTTCCCCTGATCATCAAGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAG
E--> 484  TGGAGGACCAGAAGGAGGAGGTGCAATTGCTAGTGTTCGGATTGACTGCCAACTCTGAC
```

*(handwritten: delete)*

*(handwritten: same errors)*

*(handwritten: Insert totals at end. — same errors)*

*Insert totals at the end.*

*— same errors*

```
E--> 485 ACCCACCTGCTTCAGGGGCAGAGCCTGACCCTGACCTTGGAGAGCCCCCCTGGTAGTAG
E--> 486 CCCCTCAGTGCAATGTAGGAGTCCAAGGGGTAAAAACATACAGGGGGGGAAGACCCTCT
E--> 487 CCGTGTCTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACTGTCTTGCAGAAC
E--> 488 CAGAAGAAGGTGGAGTTCAAAATAGACATCGTGGTGCTAGCTTTCCAGAAGGCCTCCAG
E--> 489 CATAGTCTATAAGAAAGAGGGGGAACAGGTGGAGTTCTCCTTCCCACTCGCCTTTACAG
E--> 490 TTGAAAAGCTGACGGGCAGTGGCGAGCTGTGGTGGCAGGCGGAGAGGGCTTCCTCCTCC
E--> 491 AAGTCTTGGATCACCTTTGACCTGAAGAACAAGGAAGTGTCTGTAAAACGGGTTACCCA
E--> 492 GGACCCTAAGCTCCAGATGGGCAAGAAGCTCCCGCTCCACCTCACCCTGCCCCAGGCCT
E--> 493 TGCCTCAGTATGCTGGCTCTGGAAACCTCACCCTGGCCCTTGAAGCGAAAACAGGAAAG
E--> 494 TTGCATCAGGAAGTGAACCTGGTGGTGATGAGAGCCACTCAGCTCCAGAAAAATTTGAC
E--> 495 CTGTGAGGTGTGGGGGACCCACCTCCCCTAAGCTGATGCTGAGCTTGAAACTGGAGAACA
E--> 496 AGGAGGCAAAGGTCTCGAAGCGGGAGAAGGCGGTGTGGGTGCTGAACCCTGAGGCGGGG
E--> 497 ATGTGGCAGTGTCTGCTGAGTGACTCGGGACAGGTCCTGCTGGAATCCAACATCAAGGT
E--> 498 TCTGCCCAGATCTAACGGTCTCCCTGGCCCCATTGGGCCCCCTGGTCCTCGCGGTCGCA
E--> 499 CTGGTGATGCTGGTCCTGTTGGTCCCCCCGGCCCTCCTGGACCTCCTGGTCCCCCTGGT
E--> 500 CCTCCCAGCGCTGGTTTCGACTTCAGCTTCCTGCCCCAGCCACCTCAAGAGAAGGCTCA
E--> 501 CGATGGTGGCCGCTACTACCGGGCTGATGATGCCAATGTGGTTCGTGACCGTGACCTCG
E--> 502 AGGTGGACACCACCCTCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAG
E--> 503 GGAAGCCGCAAGAACCCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTG
E--> 504 GAAGAGTGGAGAGTACTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAG
E--> 505 TCTTCTGCAACATGGAGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCC
E--> 506 CAGAAGAACTGGTACATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGA
E--> 507 GAGCATGACCGATGGATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATG
E--> 508 TGGCCATCCAGCTGACCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACC
E--> 509 TACCACTGCAAGAACAGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGC
E--> 510 CCTGCTCCTCAAGGGCTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCA
E--> 511 CCTACAGCGTCACTGTCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTG
E--> 512 ATTGAATACAAAACCACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCCTTGGA
E--> 513 CGTTGGTGCCCCAGACCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAA
E--> 514 CTCCCTCCATCTAGA
E--> 515          Xba I    — delete
```

```
     518 (2) INFORMATION FOR SEQ ID NO: 14:
     519     (i) SEQUENCE CHARACTERISTICS:
     520         (A) LENGTH: 699 amino acids
     521         (B) TYPE: amino acid
     522         (D) TOPOLOGY: linear
     523    (ii) MOLECULE TYPE: protein
     524    (vi) ORIGINAL SOURCE:
     525         (A) ORGANISM: Homo sapiens
     526    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14
```

*— same errors*        *— delete*

```
     529    1 MNRGVPFRHL LLVLQLALLP AATQGKKVVL GKKGDTVELT CTASQKKSIQ FHWKNSNQIK   60
     530   61 ILGNQGSFLT KGPSKLNDRA DSRRSLWDQG NFPLIIKNLK IEDSDTYICE VEDQKEEVQL  120
     531  121 LVFGLTANSD THLLQGQSLT LTLESPPGSS PSVQCRSPRG KNIQGGKTLS VSQLELQDSG  180
     532  181 TWTCTVLQNQ KKVEFKIDIV VLAFQKASSI VYKKEGEQVE FSFPLAFTVE KLTGSGELWW  240
     533  241 QAERASSSKS WITFDLKNKE VSVKRVTQDP KLQMGKKLPL HLTLPQALPQ YAGSGNLTLA  300
     534  301 LEAKTGKLHQ EVNLVVMRAT QLQKNLTCEV WGPTSPKLML SLKLENKEAK VSKREKAVWV  360
     535  361 LNPEAGMWQC LLSDSGQVLL ESNIKVLPRS NGLPGPIGPP GPRGRTGDAG PVGPPGPPGP  420
     536  421 PGPPGPPSAG FDFSFLPQPP QEKAHDGGRY YRADDANVVR DRDLEVDTTL KSLSQQIENI  480
     537  481 RSPEGSRKNP ARTCRDLKMC HSDWKSGEYW IDPNQGCNLD AIKVFCNMET GETCVYPTQP  540
```

RAW SEQUENCE LISTING                    DATE: 04/09/2004
PATENT APPLICATION: **US/10/677,877**    TIME: 15:37:16

Input Set : **A:\PTO.LN.txt**
Output Set: **N:\CRF4\04092004\J677877.raw**

*delete*

*same errors*   *delete*

```
   538.  541  SVAQKNWYIS KNPKDKRHVW FGESMTDGFQ FEYGGQGSDP ADVAIQLTFL RLMSTEASQN   600
   539   601  ITYHCKNSVA YMDQQTGNLK KALLLKGSNE IEIRAEGNSR FTYSVTVDGC TSHTGAWGKT   660
E-->  540   661  VIEYKTTKSS RLPIIDVAPL DVGAPDQEFG FDVGPVCFL
   544  (2) INFORMATION FOR SEQ ID NO: 15:
   545        (i) SEQUENCE CHARACTERISTICS:
   546            (A) LENGTH: 1947 base pairs
   547            (B) TYPE: nucleic acid
   548            (C) STRANDEDNESS: double
   549            (D) TOPOLOGY: linear
   550        (ii) MOLECULE TYPE: cDNA
W-->  551       (iii) HYPOTHETICAL: N
W-->  552       (iv) ANTI-SENSE: N
   553        (vi) ORIGINAL SOURCE:
   554            (A) ORGANISM: Homo sapiens
   556       (vii) IMMEDIATE SOURCE:
   557            (B) CLONE: pTrimer/sCD4-T2
   558        (ix) FEATURE:
   559            (A) NAME/KEY: CDS
   560            (B) LOCATION: 24..1931
   561            (D) OTHER INFORMATION:
   562        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15
E-->  565  Hind III   delete
```

*Insert totals at the end.*   *59*

```
E-->  566  AAGCTTCCCTCGGCAAGGCCACAATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTG
E-->  567  GTGCTGCAACTGGCGCTCCTCCCAGCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAA
E-->  568  AAAAGGGGATACAGTGGAACTGACCTGTACAGCTTCCCAGAAGAAGAGCATACAATTCC
E-->  569  ACTGGAAAAACTCCAACCAGATAAAGATTCTGGGAAATCAGGGCTCCTTCTTAACTAAA
E-->  570  GGTCCATCCAAGCTGAATGATCGCGCTGACTCAAGAAGAAGCCTTTGGGACCAAGGAAA
E-->  571  CTTTCCCCTGATCATCAAGAATCTTAAGATAGAAGACTCAGATACTTACATCTGTGAAG
E-->  572  TGGAGGACCAGAAGGAGGAGGTGCAATTGCTAGTGTTCGGATTGACTGCCAACTCTGAC
E-->  573  ACCCACCTGCTTCAGGGGCAGAGCCTGACCCTGACCTTGGAGAGCCCCCCTGGTAGTAG
E-->  574  CCCCTCAGTGCAATGTAGGAGTCCAAGGGGTAAAAACATACAGGGGGGGGAAGACCCTCT
E-->  575  CCGTGTCTCAGCTGGAGCTCCAGGATAGTGGCACCTGGACATGCACTGTCTTGCAGAAC
E-->  576  CAGAAGAAGGTGGAGTTCAAAATAGACATCGTGGTGCTAGCTTTCCAGAAGGCCTCCAG
E-->  577  CATAGTCTATAAGAAAGAGGGGGAACAGGTGGAGTTCTCCTTCCCACTCGCCTTTACAG
E-->  578  TTGAAAAGCTGACGGGCAGTGGCGAGCTGTGGTGGCAGGCGGAGAGGGCTTCCTCCTCC
E-->  579  AAGTCTTGGATCACCTTTGACCTGAAGAACAAGGAAGTGTCTGTAAAACGGGTTACCCA
E-->  580  GGACCCTAAGCTCCAGATGGGCAAGAAGCTCCCGCTCCACCTCACCCTGCCCCAGGCCT
E-->  581  TGCCTCAGTATGCTGGCTCTGGAAACCTCACCCTGGCCCTTGAAGCGAAAACAGGAAAG
E-->  582  TTGCATCAGGAAGTGAACCTGGTGGTGATGAGAGCCACTCAGCTCCAGAAAAATTTGAC
E-->  583  CTGTGAGGTGTGGGGGACCCACCTCCCCTAAGCTGATGCTGAGCTTGAAACTGGAGAACA
E-->  584  AGGAGGCAAAGGTCTCGAAGCGGGAGAAGGCGGTGTGGGTGCTGAACCCTGAGGCGGGG
E-->  585  ATGTGGCAGTGTCTGCTGAGTGACTCGGGACAGGTCCTGCTGGAATCCAACATCAAGGT
E-->  586  TCTGCCCAGATCTGATGCCAATGTGGTTCGTGACCGTGACCTCGAGGTGGACACCACCC
E-->  587  TCAAGAGCCTGAGCCAGCAGATCGAGAACATCCGGAGCCCAGAGGGAAGCCGCAAGAAC
E-->  588  CCCGCCCGCACCTGCCGTGACCTCAAGATGTGCCACTCTGACTGGAAGAGTGGAGAGTA
E-->  589  CTGGATTGACCCCAACCAAGGCTGCAACCTGGATGCCATCAAAGTCTTCTGCAACATGG
E-->  590  AGACTGGTGAGACCTGCGTGTACCCCACTCAGCCCAGTGTGGCCCAGAAGAACTGGTAC
E-->  591  ATCAGCAAGAACCCCAAGGACAAGAGGCATGTCTGGTTCGGCGAGAGCATGACCGATGG
E-->  592  ATTCCAGTTCGAGTATGGCGGCCAGGGCTCCGACCCTGCCGATGTGGCCATCCAGCTGA
```

*same errors*

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/677,877**

DATE: 04/09/2004
TIME: 15:37:16

*Insert totals*

Input Set : **A:\PTO.LN.txt**
Output Set: **N:\CRF4\04092004\J677877.raw**

*same errors*

```
E--> 593  CCTTCCTGCGCCTGATGTCCACCGAGGCCTCCCAGAACATCACCTACCACTGCAAGAAC
E--> 594  AGCGTGGCCTACATGGACCAGCAGACTGGCAACCTCAAGAAGGCCCTGCTCCTCAAGGG
E--> 595  CTCCAACGAGATCGAGATCCGCGCCGAGGGCAACAGCCGCTTCACCTACAGCGTCACTG
E--> 596  TCGATGGCTGCACGAGTCACACCGGAGCCTGGGGCAAGACAGTGATTGAATACAAAACC
E--> 597  ACCAAGTCCTCCCGCCTGCCCATCATCGATGTGGCCCCCTTGGACGTTGGTGCCCCAGA
E--> 598  CCAGGAATTCGGCTTCGACGTTGGCCCTGTCTGCTTCCTGTAAACTCCCTCCATCTAGA
E--> 599        Xba I  —delete
```

```
     602  (2) INFORMATION FOR SEQ ID NO: 16:
     603       (i) SEQUENCE CHARACTERISTICS:
     604           (A) LENGTH: 635 amino acids
     605           (B) TYPE: amino acid
     606           (D) TOPOLOGY: linear
     607  (ii) MOLECULE TYPE: protein
     608  (vi) ORIGINAL SOURCE:
     609           (A) ORGANISM: Homo sapiens
     610       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16
```

*same errors*         *delete*

```
     613    1 MNRGVPFRHL LLVLQLALLP AATQGKKVVL GKKGDTVELT CTASQKKSIQ FHWKNSNQIK   60
     614   61 ILGNQGSFLT KGPSKLNDRA DSRRSLWDQG NFPLIIKNLK IEDSDTYICE VEDQKEEVQL  120
     615  121 LVFGLTANSD THLLQGQSLT LTLESPPGSS PSVQCRSPRG KNIQGGKTLS VSQLELQDSG  180
     616  181 TWTCTVLQNQ KKVEFKIDIV VLAFQKASSI VYKKEGEQVE FSFPLAFTVE KLTGSGELWW  240
     617  241 QAERASSSKS WITFDLKNKE VSVKRVTQDP KLQMGKKLPL HLTLPQALPQ YAGSGNLTLA  300
     618  301 LEAKTGKLHQ EVNLVVMRAT QLQKNLTCEV WGPTSPKLML SLKLENKEAK VSKREKAVWV  360
     619  361 LNPEAGMWQC LLSDSGQVLL ESNIKVLPRS DANVVRDRDL EVDTTLKSLS QQIENIRSPE  420
     620  421 GSRKNPARTC RDLKMCHSDW KSGEYWIDPN QGCNLDAIKV FCNMETGETC VYPTQPSVAQ  480
     621  481 KNWYISKNPK DKRHVWFGES MTDGFQFEYG GQGSDPADVA IQLTFLRLMS TEASQNITYH  540
     622  541 CKNSVAYMDQ QTGNLKKALL LKGSNEIEIR AEGNSRFTYS VTVDGCTSHT GAWGKTVIEY  600
E--> 623  601 KTTKSSRLPI IDVAPLDVGA PDQEFGFDVG PVCFL
```

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**VERIFICATION SUMMARY**
PATENT APPLICATION: **US/10/677,877**

DATE: 04/09/2004
TIME: 15:37:17

Input Set : **A:\PTO.LN.txt**
Output Set: **N:\CRF4\04092004\J677877.raw**

```
L:0 M:200 E: Mandatory Header Field missing, [(i) APPLICANT:] of (1)
L:0 M:200 E: Mandatory Header Field missing, [(ii) TITLE OF INVENTION:] of (1)
L:0 M:200 E: Mandatory Header Field missing, [(A) ADDRESSEE:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(B) STREET:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(C) CITY:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(D) STATE:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(E) COUNTRY:] of (1)(iv)
L:0 M:200 E: Mandatory Header Field missing, [(F) ZIP:] of (1)(iv)
L:0 M:249 C: Inserted Mandatory Field, [(vi) CURRENT APPLICATION DATA:]
L:0 M:249 C: Inserted Mandatory Field, [(A) APPLICATION NUMBER:]
L:0 M:249 C: Inserted Mandatory Field, [(B) FILING DATE:]
L:13 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=1
L:14 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=1
L:27 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:27 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:28 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:28 M:254 E: No. of Bases conflict, Input:0 Counted:55 SEQ:1
M:254 Repeated in SeqNo=1
L:46 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:46 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:64 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:64 M:330 E: (2) Invalid Amino Acid Designator, 2
L:64 M:203 E: No. of Seq. differs, LENGTH:Input:311 Found:2 SEQ:2
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=3
L:75 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=3
L:88 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
L:88 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:89 M:254 E: No. of Bases conflict, Input:0 Counted:64 SEQ:3
M:254 Repeated in SeqNo=3
L:102 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:102 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:120 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:120 M:330 E: (2) Invalid Amino Acid Designator, 1
L:120 M:203 E: No. of Seq. differs, LENGTH:Input:247 Found:1 SEQ:4
L:130 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=5
L:131 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=5
L:144 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:144 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:145 M:254 E: No. of Bases conflict, Input:0 Counted:59 SEQ:5
M:254 Repeated in SeqNo=5
L:188 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:188 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:215 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:215 M:330 E: (2) Invalid Amino Acid Designator, 4
L:215 M:203 E: No. of Seq. differs, LENGTH:Input:819 Found:4 SEQ:6
L:225 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=7
L:226 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=7
```

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```
L:238 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:238 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:239 M:254 E: No. of Bases conflict, Input:0 Counted:59 SEQ:7
M:254 Repeated in SeqNo=7
L:278 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:278 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:304 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:304 M:330 E: (2) Invalid Amino Acid Designator, 4
L:304 M:203 E: No. of Seq. differs, LENGTH:Input:755 Found:4 SEQ:8
L:314 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=9
L:315 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=9
L:327 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:327 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:328 M:254 E: No. of Bases conflict, Input:0 Counted:64 SEQ:9
M:254 Repeated in SeqNo=9
L:357 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:357 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:380 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:380 M:330 E: (2) Invalid Amino Acid Designator, 3
L:380 M:203 E: No. of Seq. differs, LENGTH:Input:566 Found:3 SEQ:10
L:390 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=11
L:391 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=11
L:404 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:404 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:405 M:254 E: No. of Bases conflict, Input:0 Counted:64 SEQ:11
M:254 Repeated in SeqNo=11
L:431 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:431 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:453 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:453 M:330 E: (2) Invalid Amino Acid Designator, 3
L:453 M:203 E: No. of Seq. differs, LENGTH:Input:502 Found:3 SEQ:12
L:463 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=13
L:464 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=13
L:477 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:477 M:333 E: Wrong sequence grouping, Amino acids not in groups
L:478 M:254 E: No. of Bases conflict, Input:0 Counted:59 SEQ:13
M:254 Repeated in SeqNo=13
L:515 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:515 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:540 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:540 M:330 E: (2) Invalid Amino Acid Designator, 4
L:540 M:203 E: No. of Seq. differs, LENGTH:Input:699 Found:4 SEQ:14
L:551 M:246 W: Invalid value of Alpha Sequence Header Field, [HYPOTHETICAL:], SeqNo=15
L:552 M:246 W: Invalid value of Alpha Sequence Header Field, [ANTI-SENSE:], SeqNo=15
L:565 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
L:565 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:566 M:254 E: No. of Bases conflict, Input:0 Counted:59 SEQ:15
M:254 Repeated in SeqNo=15
L:599 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
```

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Input Set : **A:\PTO.LN.txt**
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L:599 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:623 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:623 M:330 E: (2) Invalid Amino Acid Designator, 4
L:623 M:203 E: No. of Seq. differs, LENGTH:Input:635 Found:4 SEQ:16